Sequence listing

<110> SHANGHAI CANCER INSTITUTE

<120> A HUMAN TUMOR-ASSOCIATED GENE CT120 ON CHROMOSOME 17P 13.3 REGION AND PROTEIN ENCODED BY IT

<130> 024832pc

<140> US 10/536,772
<141> 2005-05-26

<150> CN 02150730.9
<151> 2002-11-27

<160> 13

<170> PatentIn version 3.1

<210> 1
<211> 2145
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (91)..(861)
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<400> 1

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gccagcgagg cggccggacc cgcagccccg atg ctg ctg acg ctg gcc ggg ggc     114
                                Met Leu Leu Thr Leu Ala Gly Gly
                                1               5
gcg ctc ttc ttc ccg ggg ctc ttc gcg ctc tgc acc tgg gcg ctg cgc      162
Ala Leu Phe Phe Pro Gly Leu Phe Ala Leu Cys Thr Trp Ala Leu Arg
    10                  15                  20
cac tcc cag ccc gga tgg agc cgc acc gac tgc gtg atg atc agc acc      210
His Ser Gln Pro Gly Trp Ser Arg Thr Asp Cys Val Met Ile Ser Thr
25                  30                  35                  40
agg ctg gtt tcc tcg gtg cac gcc gtg ctg gcc acc ggc tcg ggg atc      258
Arg Leu Val Ser Ser Val His Ala Val Leu Ala Thr Gly Ser Gly Ile
                45                  50                  55
gtc atc att cgc tcc tgc gac gac gtg atc acc ggc agg cac tgg ctt      306
Val Ile Ile Arg Ser Cys Asp Asp Val Ile Thr Gly Arg His Trp Leu
            60                  65                  70
gcc cgg gaa tat gtg tgg ttt ctg att cca tac atg atc tat gac tcg      354
Ala Arg Glu Tyr Val Trp Phe Leu Ile Pro Tyr Met Ile Tyr Asp Ser
        75                  80                  85
tac gcc atg tac ctc tgt gaa tgg tgc cga acc aga gac cag aac cgt      402
Tyr Ala Met Tyr Leu Cys Glu Trp Cys Arg Thr Arg Asp Gln Asn Arg
    90                  95                  100
gcg ccc tcc ctc act ctt cga aac ttc cta agt cga aac cgc ctc atg      450
Ala Pro Ser Leu Thr Leu Arg Asn Phe Leu Ser Arg Asn Arg Leu Met
105                 110                 115                 120
atc aca cat cat gcg gtc att ctc ctt gtc ctt gtg cca gtc gca cag      498
Ile Thr His His Ala Val Ile Leu Leu Val Leu Val Pro Val Ala Gln
                125                 130                 135
agg ctc cgg gga gac ctt ggg gac ttc ttt gtc ggc tgc atc ttc acg      546
Arg Leu Arg Gly Asp Leu Gly Asp Phe Phe Val Gly Cys Ile Phe Thr
            140                 145                 150
gca gaa ctg agc act ccg ttt gtg tcg ctg ggc agg gtt ctg att cag      594
Ala Glu Leu Ser Thr Pro Phe Val Ser Leu Gly Arg Val Leu Ile Gln
        155                 160                 165
cta aag cag cag cac acc ctt ctg tac aag gtg aat gga atc ctc acg      642
Leu Lys Gln Gln His Thr Leu Leu Tyr Lys Val Asn Gly Ile Leu Thr
    170                 175                 180
ctg gcc acc ttc ctt tcc tgc cgg atc ctt ctc ttc ccc ttc atg tac      690
Leu Ala Thr Phe Leu Ser Cys Arg Ile Leu Leu Phe Pro Phe Met Tyr
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185                 190                 195                 200
tgg tcc tat ggc cgc cag cag gga cta agc ctg ctc caa gta ccc ttc      738
Trp Ser Tyr Gly Arg Gln Gln Gly Leu Ser Leu Leu Gln Val Pro Phe
                205                 210                 215
agc atc cca ttc tac tgc aac gtg gcc aat gcc ttc ctc gta gct cct      786
Ser Ile Pro Phe Tyr Cys Asn Val Ala Asn Ala Phe Leu Val Ala Pro
            220                 225                 230
cag atc tac tgg ttc tgt ctg ctg tgc agg aag gca gtc cgg ctc ttt      834
Gln Ile Tyr Trp Phe Cys Leu Leu Cys Arg Lys Ala Val Arg Leu Phe
        235                 240                 245
gac act ccc caa gcc aaa aag gat ggc taaatgctcc tgggagtcag            881
Asp Thr Pro Gln Ala Lys Lys Asp Gly
    250                 255
gcgcagcctc acaccagctg cctcctccac tcagcattcc atggaccaaa ttgtgccctg    941
ggtagcctca gactttgggt attgataagc cgatggattt gagtttttct aaagaatatt   1001
catattacct ccttttttcta acttgcccta tttgcaaacg cacttttgta gtaacaacta   1061
ttgggtcctg tcagacctcc acggacagca aagtggtttt aatgcaagcc caaggatcct   1121
tcttaaggtc ttatctcaag agctctggga ggtggaagca tggggtggga tcggtggacc   1181
agggtggtaa gtgtctgcac atctgcctgt ccctgtatca gcggctaccc accttccaaa   1241
ccactcagga cagtacccgt ggcactgggc ccgcagaagc aagggatgac ttggttcttg   1301
gaagtaatgt cgtcttgtga cattggcctg ggacaatcat tgtgggtagg tagttattga   1361
tcgtttacta gataacccat tggttctttg cctcatcctc tcatccatgg gtcagagttg   1421
aattcttatg tctatagact tccaatcaga agtctcactg gtggggctgg gggtgggggc   1481
aggcaggagg catggatggg aacctgagta ggtagtgtgg ccaagagatc agcacaacct   1541
ttgcaggctg acttgctaag tctgacagtg acaaacttgt gagcttactg cagtcagtca   1601
cagaggctgt tctttttcac acaccccttc atgcccggct ttccccatat ccacatgcag   1661
agggcgagct cataaaacta cagggaagcg tgaaatgatg gctttggtag ctgtttactg   1721
ggtaacccca ctgtgacact gtccttttca tgtgatgtgg aaacctactt ctgtcctcca   1781
aaccatgaaa tgtgtcatct agactgcaga gtactcgagt gctttgcctc ccgatatgcc   1841
agagcttgtg gtccaaagcc cattcctgtg tgtccgtcct gccatttagc cacagaaggc   1901
tgcggagtga ggcggcagct agcctggcca gtggctgtcc cgtggaccga cacctgcgcc   1961
cccttctgca agcaggattt tctggtgcca acactcattc atcattcccg atcaactagg   2021
atgaatttaa gactgtgcta ccatgtgttc tcaagtggta gtttaaaaag tggattttta   2081
aagtgccttt caattgtctg tgaacgtcta aaggactgat ttgtctcaaa aaaaaaaaaa   2141
aaaa                                                                2145

<210>  2
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<212>  PRT
<213>  Homo sapiens

<400>  2
Met Leu Leu Thr Leu Ala Gly Gly Ala Leu Phe Phe Pro Gly Leu Phe
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Ala Leu Cys Thr Trp Ala Leu Arg His Ser Gln Pro Gly Trp Ser Arg
            20                  25                  30
Thr Asp Cys Val Met Ile Ser Thr Arg Leu Val Ser Ser Val His Ala
        35                  40                  45
Val Leu Ala Thr Gly Ser Gly Ile Val Ile Ile Arg Ser Cys Asp Asp
    50                  55                  60
Val Ile Thr Gly Arg His Trp Leu Ala Arg Glu Tyr Val Trp Phe Leu
65                  70                  75                  80
Ile Pro Tyr Met Ile Tyr Asp Ser Tyr Ala Met Tyr Leu Cys Glu Trp
                85                  90                  95
Cys Arg Thr Arg Asp Gln Asn Arg Ala Pro Ser Leu Thr Leu Arg Asn
            100                 105                 110
Phe Leu Ser Arg Asn Arg Leu Met Ile Thr His His Ala Val Ile Leu
        115                 120                 125
Leu Val Leu Val Pro Val Ala Gln Arg Leu Arg Gly Asp Leu Gly Asp
    130                 135                 140
Phe Phe Val Gly Cys Ile Phe Thr Ala Glu Leu Ser Thr Pro Phe Val
145                 150                 155                 160
Ser Leu Gly Arg Val Leu Ile Gln Leu Lys Gln Gln His Thr Leu Leu
                165                 170                 175
Tyr Lys Val Asn Gly Ile Leu Thr Leu Ala Thr Phe Leu Ser Cys Arg
            180                 185                 190
Ile Leu Leu Phe Pro Phe Met Tyr Trp Ser Tyr Gly Arg Gln Gln Gly
        195                 200                 205
Leu Ser Leu Leu Gln Val Pro Phe Ser Ile Pro Phe Tyr Cys Asn Val
    210                 215                 220
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Ala Asn Ala Phe Leu Val Ala Pro Gln Ile Tyr Trp Phe Cys Leu Leu
225 230 235 240
Cys Arg Lys Ala Val Arg Leu Phe Asp Thr Pro Gln Ala Lys Lys Asp
245 250 255
Gly

<210> 3
<211> 25
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<222> (1)..(25)
<223> primer

<400> 3
gtgcgactgg cacaaggaca aagag 25

<210> 4
<211> 23
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<222> (1)..(23)
<223> primer

<400> 4
cgaatgatga cgatccccga gcc 23

<210> 5
<211> 22
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<222> (1)..(22)
<223> primer

<400> 5
ccgatgctgc tgacgctggc cg 22

<210> 6
<211> 25
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<222> (1)..(25)
<223> primer

<400> 6
tgttggcacc agaaaatcct gcttg 25

<210> 7
<211> 20
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<222> (1)..(20)
<223> primer

<400> 7

aagtactccg tgtggatcgg 20

<210> 8
<211> 20
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<222> (1)..(20)
<223> primer

<400> 8
tcaagttggg ggacaaaaag 20

<210> 9
<211> 25
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<222> (1)..(25)
<223> primer

<400> 9
gtgcgactgg cacaaggaca aagag 25

<210> 10
<211> 23
<212> DNA
<213> Artificial

<220>
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<222> (1)..(23)
<223> primer

<400> 10
ggggatcgtc atcattcgct cct 23

<210> 11
<211> 15
<212> PRT
<213> Artificial

<220>
<221> MISC_FEATURE
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<223> oligopeptide corresponding to C-terminus of CT120 protein

<400> 11

Cys Arg Lys Ala Val Arg Leu Phe Asp Thr Pro Gln Ala Lys Lys
1 5 10 15

<210> 12
<211> 20
<212> DNA
<213> Artificial

<220>
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<222> (1)..(20)
<223> primer

<400> 12
atgctgctga cgctggccgg 20

<210> 13

<211> 20
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<213> Artificial

<220>
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<223> primer

<400> 13
ttagccatcc tttttggctt 20

<210> 14
<211> 224
<212> PRT
<213> Homo sapiens

<400> 14

Met Ala Ser Thr Ala Gly Tyr Ile Val Ser Thr Ser Cys Lys His Ile
1 5 10 15
Ile Asp Asp Gln His Trp Leu Ser Ser Ala Tyr Thr Gln Phe Ala Val
20 25 30
Pro Tyr Phe Ile Tyr Asp Ile Tyr Ala Met Phe Leu Cys His Trp His
35 40 45
Lys His Gln Val Lys Gly His Gly Gly Asp Asp Gly Ala Ala Arg Ala
50 55 60
Pro Gly Ser Thr Trp Ala Ile Ala Arg Gly Tyr Leu His Lys Glu Phe
65 70 75 80
Leu Met Val Leu His His Ala Ala Met Val Leu Val Cys Phe Pro Leu
85 90 95
Ser Val Val Trp Arg Gln Gly Lys Gly Asp Phe Phe Leu Gly Cys Met
100 105 110
Leu Met Ala Glu Val Ser Thr Pro Phe Val Cys Leu Gly Lys Ile Leu
115 120 125
Ile Gln Tyr Lys Gln Gln His Thr Leu Leu His Lys Val Asn Gly Ala
130 135 140
Leu Met Leu Leu Ser Phe Leu Cys Cys Arg Val Leu Leu Phe Pro Tyr
145 150 155 160
Leu Tyr Trp Ala Tyr Gly Arg His Ala Gly Leu Pro Leu Leu Ala Val
165 170 175
Pro Leu Ala Ile Pro Ala His Val Asn Leu Gly Ala Ala Leu Leu Leu
180 185 190
Ala Pro Gln Leu Tyr Trp Phe Phe Leu Ile Cys Arg Gly Ala Cys Arg
195 200 205
Leu Phe Trp Pro Arg Ser Arg Pro Pro Pro Ala Cys Gln Ala Gln Asp
210 215 220

<210> 15
<211> 275
<212> PRT
<213> Homo sapiens

<400> 15

Met Leu Thr Pro Met Val Ala Gly Gly Val Val Phe Pro Gly Leu Phe
1 5 10 15
Leu Leu Ser Lys Asn Thr Leu Gln Arg Leu Pro Gln Leu Arg Trp Glu
20 25 30
Glu Ala Asp Ala Val Ile Val Ser Ala Arg Leu Val Ser Ser Val Gln
35 40 45
Ala Ile Met Ala Ser Thr Ala Gly Tyr Ile Val Ser Thr Ser Cys Lys
50 55 60
His Ile Ile Asp Asp Gln His Trp Leu Ser Ser Ala Tyr Thr Gln Phe
65 70 75 80
Ala Val Pro Tyr Phe Ile Tyr Asp Ile Tyr Ala Met Phe Leu Cys His
85 90 95
Trp His Lys His Gln Val Lys Gly His Gly Gly Glu Asp Gly Thr Pro
100 105 110

```
Arg Ala Leu Gly Ser Thr Trp Ala Val Val Arg Gly Tyr Leu His Lys
        115                 120                 125
Glu Phe Leu Met Val Leu His His Ala Ala Met Val Leu Val Cys Phe
    130                 135                 140
Pro Leu Ser Val Val Trp Arg Gln Gly Lys Gly Asp Phe Phe Leu Gly
145                 150                 155                 160
Cys Met Leu Met Ala Glu Val Ser Thr Pro Phe Val Cys Leu Gly Lys
                165                 170                 175
Ile Leu Ile Gln Tyr Lys Gln Gln His Thr Leu Leu His Lys Val Asn
            180                 185                 190
Gly Ala Leu Met Leu Leu Ser Phe Leu Cys Cys Arg Val Leu Leu Phe
        195                 200                 205
Pro Tyr Leu Tyr Trp Ala Tyr Gly Arg His Ala Gly Leu Pro Leu Leu
    210                 215                 220
Ser Val Pro Met Ala Ile Pro Ala His Val Asn Leu Gly Ala Ala Leu
225                 230                 235                 240
Leu Leu Ala Pro Gln Leu Tyr Trp Phe Phe Leu Ile Cys Arg Gly Ala
                245                 250                 255
Cys Arg Leu Phe Arg Pro Arg Gly Ser Pro Pro Pro Ser Pro Cys Gln
            260                 265                 270
Thr Gln Asp
        275
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<210> 16
<211> 353
<212> PRT
<213> Homo sapiens

<400> 16

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Leu Ala Ile Pro Ser Ser Pro Pro Thr Pro Ser Leu Asn Leu Ala Phe
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Leu Ser Leu Leu Asp Pro Leu Val Ser Leu Pro Gly Phe Lys Ser Pro
            20                  25                  30
Cys Leu Pro Gln Trp Trp Leu Gly Gly Trp Cys Ser Pro Asp Ser Ser
        35                  40                  45
Ser Tyr Pro Arg Thr Arg Ser Arg Gly Cys Pro Ser Cys Ala Gly Arg
    50                  55                  60
Glu Ala Asp Ala Val Ile Val Ser Ala Arg Leu Val Ser Ser Val Gln
65                  70                  75                  80
Ala Ile Met Ala Ser Thr Ala Gly Tyr Ile Val Ser Thr Ser Cys Lys
                85                  90                  95
His Ile Ile Asp Asp Gln His Trp Leu Ser Ser Ala Tyr Thr Gln Phe
            100                 105                 110
Ala Val Pro Tyr Phe Ile Tyr Asp Ile Tyr Ala Met Phe Leu Cys His
        115                 120                 125
Trp His Lys His Gln Val Lys Gly His Gly Gly Glu Asp Gly Thr Pro
    130                 135                 140
Arg Ala Leu Gly Ser Thr Trp Ala Val Val Arg Gly Tyr Leu His Lys
145                 150                 155                 160
Glu Phe Leu Met Val Leu His His Ala Ala Met Val Leu Val Cys Phe
                165                 170                 175
Pro Leu Ser Val Val Trp Arg Gln Gly Lys Gly Asp Phe Phe Leu Gly
            180                 185                 190
Cys Met Leu Met Ala Glu Val Ser Thr Pro Phe Val Cys Leu Gly Lys
        195                 200                 205
Ile Leu Ile Gln Tyr Lys Gln Gln His Thr Leu Leu His Lys Val Asn
    210                 215                 220
Gly Ala Leu Met Leu Leu Ser Phe Leu Cys Cys Arg Val Leu Leu Phe
225                 230                 235                 240
Pro Thr Cys Thr Gly Pro Thr Gly Ala Thr Leu Ala Cys Pro Cys Ser
                245                 250                 255
Gln Cys Pro Trp Pro Ser Cys Ala Thr Ser Thr Trp Ala Arg Thr Ala
            260                 265                 270
Pro Arg Thr Gln Leu Tyr Trp Leu Ser Leu Met Cys Arg Gly Asp Cys
        275                 280                 285
Gly Leu Phe Arg Pro Arg Ala Pro Thr His Pro Leu Leu Val Arg Pro
    290                 295                 300
Arg Thr Glu Ala Arg Pro Trp Asn Pro Pro Pro Pro Pro Ala Pro Val
305                 310                 315                 320
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Glu Thr Val His Trp Gly Asn Gln Cys Val Ser Trp Gly Gly Gly Asp
                325                 330                 335
Glu Ser Gln Lys Ser Leu Ser Leu Thr Ala Pro Arg Gln Met Asp Leu
            340                 345                 350
Glu
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<210> 17
<211> 257
<212> PRT
<213> Mus musculus

<400> 17

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Met Leu Leu Thr Leu Ala Gly Gly Ala Leu Phe Phe Pro Gly Leu Phe
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Ala Leu Cys Thr Trp Ala Leu Arg Arg Ser Gln Pro Gly Trp Ser Arg
            20                  25                  30
Thr Asp Cys Val Met Ile Ser Thr Arg Leu Val Ser Ser Val His Ala
        35                  40                  45
Val Leu Ala Thr Gly Ser Gly Ile Val Ile Ile Arg Ser Cys Asp Asp
    50                  55                  60
Val Ile Thr Gly Arg His Trp Leu Ala Arg Glu Tyr Val Trp Phe Leu
65                  70                  75                  80
Ile Pro Tyr Met Ile Tyr Asp Ser Tyr Ala Met Tyr Leu Cys Glu Trp
                85                  90                  95
Cys Arg Thr Arg Asp Gln Asn Arg Ala Pro Ser Leu Thr Leu Arg Asn
            100                 105                 110
Phe Leu Ser Arg Asn Arg Leu Met Ile Thr His His Ala Val Ile Leu
        115                 120                 125
Phe Val Leu Val Pro Val Ala Gln Arg Leu Arg Gly Asp Leu Gly Asp
    130                 135                 140
Phe Phe Val Gly Cys Ile Phe Thr Ala Glu Leu Ser Thr Pro Phe Val
145                 150                 155                 160
Ser Leu Gly Arg Val Leu Ile Gln Leu Lys Gln Gln His Thr Leu Leu
                165                 170                 175
Tyr Lys Val Asn Gly Ile Leu Thr Leu Ala Thr Phe Leu Ser Cys Arg
            180                 185                 190
Ile Leu Leu Phe Pro Phe Met Tyr Trp Ser Tyr Gly Arg Gln Gln Gly
        195                 200                 205
Leu Ser Leu Leu Gln Val Pro Phe Ser Ile Pro Phe Tyr Cys Asn Val
    210                 215                 220
Ala Asn Ala Phe Leu Val Ala Pro Gln Ile Tyr Trp Phe Cys Leu Leu
225                 230                 235                 240
Cys Arg Lys Ala Val Arg Leu Phe Asp Thr Pro Gln Ala Lys Lys Asp
                245                 250                 255
Gly
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<210> 18
<211> 225
<212> PRT
<213> Mus musculus

<400> 18

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Met Leu Leu Thr Leu Ala Gly Gly Ala Leu Phe Phe Pro Gly Leu Phe
1               5                  10                  15
Ala Leu Cys Thr Trp Ala Leu Arg Arg Ser Gln Pro Gly Trp Ser Arg
            20                  25                  30
Thr Asp Cys Val Met Ile Ser Thr Arg Leu Val Ser Ser Val His Ala
        35                  40                  45
Val Leu Ala Thr Gly Ser Gly Ile Val Ile Ile Arg Ser Cys Asp Asp
    50                  55                  60
Val Ile Thr Gly Arg His Trp Leu Ala Arg Glu Tyr Val Trp Phe Leu
65                  70                  75                  80
Ile Pro Tyr Met Ile Tyr Asp Ser Tyr Ala Met Tyr Leu Cys Glu Trp
                85                  90                  95
Cys Arg Thr Arg Asp Gln Asn Arg Ala Pro Ser Leu Thr Leu Arg Asn
            100                 105                 110
Phe Leu Ser Arg Asn Arg Leu Met Ile Thr His His Ala Val Ile Leu
```

```
        115                 120                 125
Phe Val Leu Val Pro Val Ala Gln Leu Lys Gln Gln His Thr Leu Leu
    130                 135                 140
Tyr Lys Val Asn Gly Ile Leu Thr Leu Ala Thr Phe Leu Ser Cys Arg
145                 150                 155                 160
Ile Leu Leu Phe Pro Phe Met Tyr Trp Ser Tyr Gly Arg Gln Gln Gly
                165                 170                 175
Leu Ser Leu Leu Gln Val Pro Phe Ser Ile Pro Phe Tyr Cys Asn Val
            180                 185                 190
Ala Asn Ala Phe Leu Val Ala Pro Gln Ile Tyr Trp Phe Cys Leu Leu
        195                 200                 205
Cys Arg Lys Ala Val Arg Leu Phe Asp Thr Pro Gln Ala Lys Lys Asp
    210                 215                 220
Gly
225
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